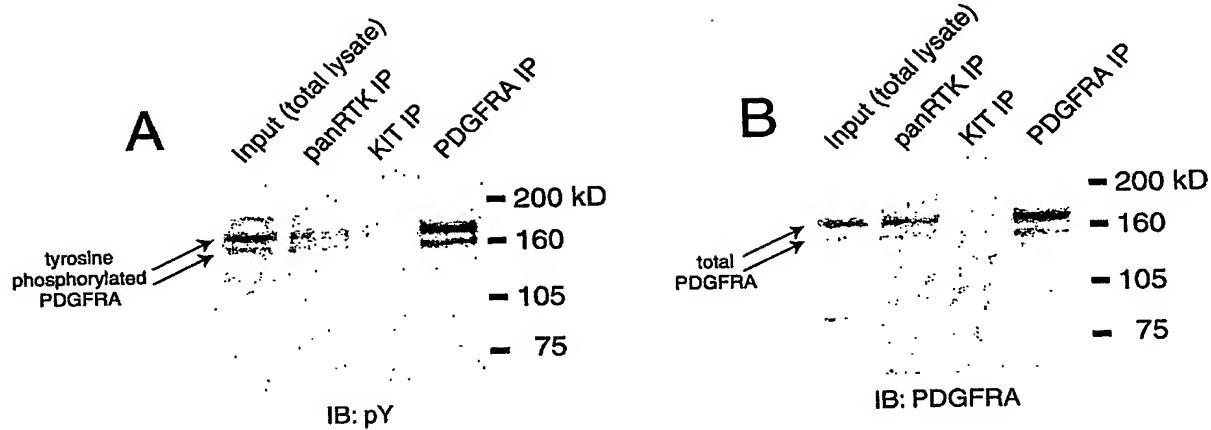


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## FIGURE 1



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FIGURE 2A

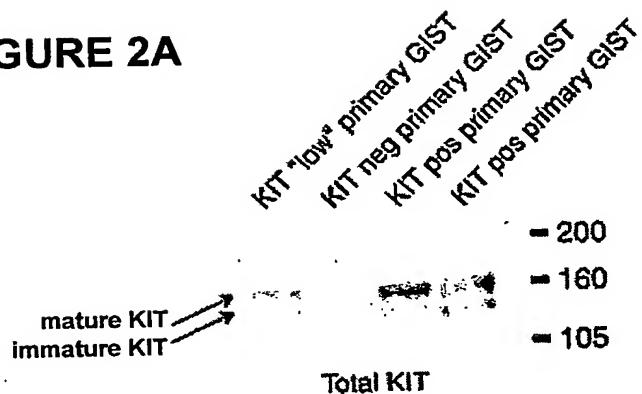


FIGURE 2B

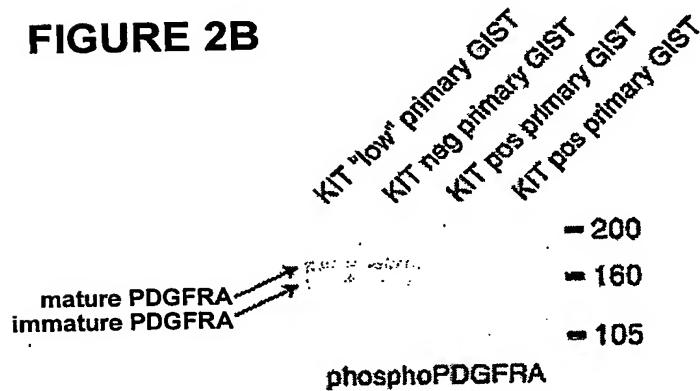
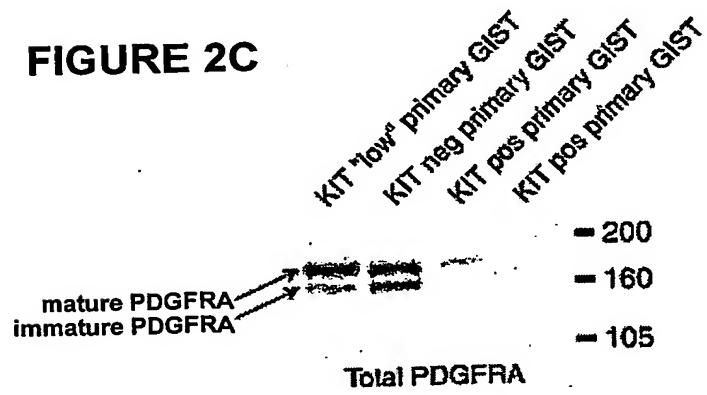


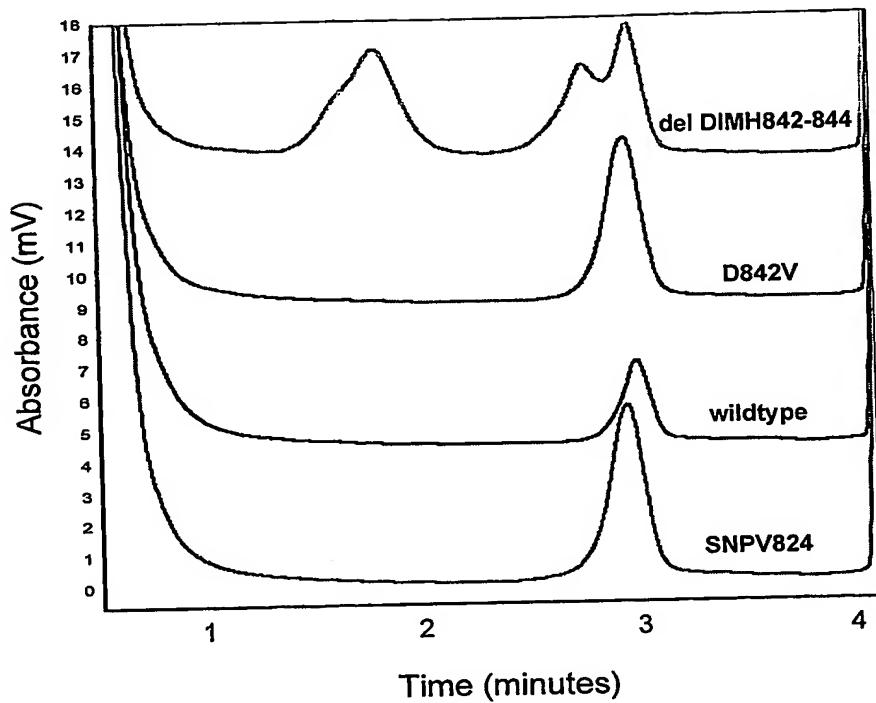
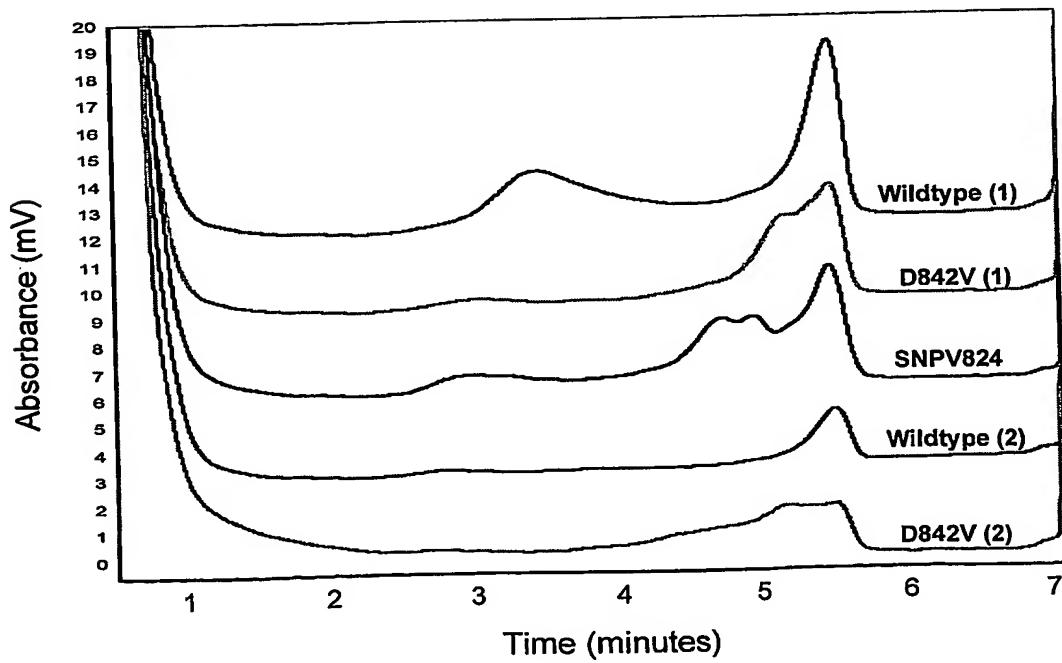
FIGURE 2C



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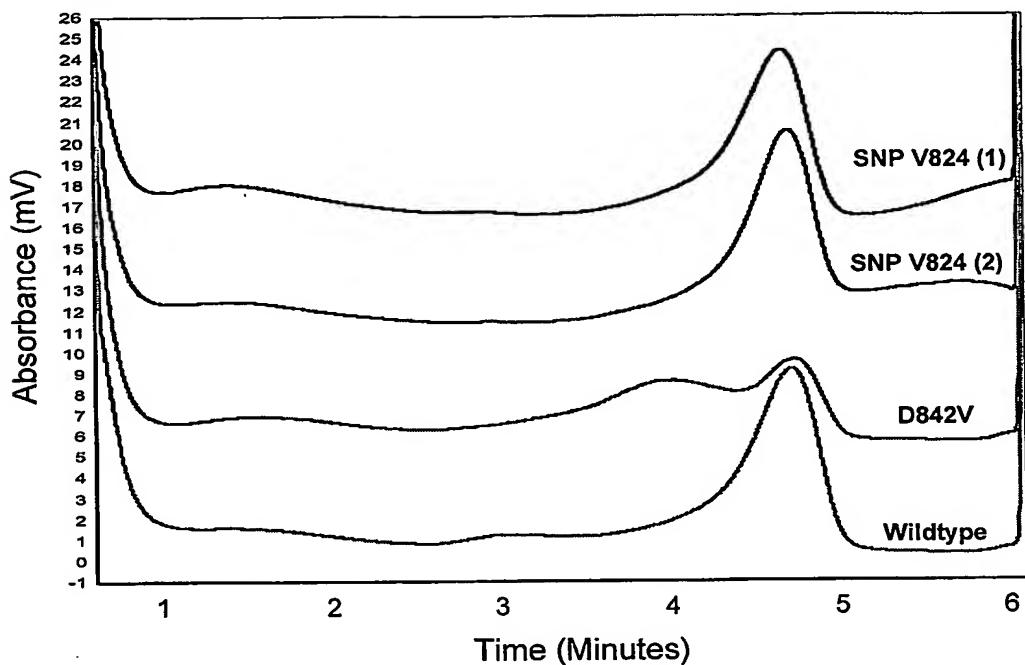
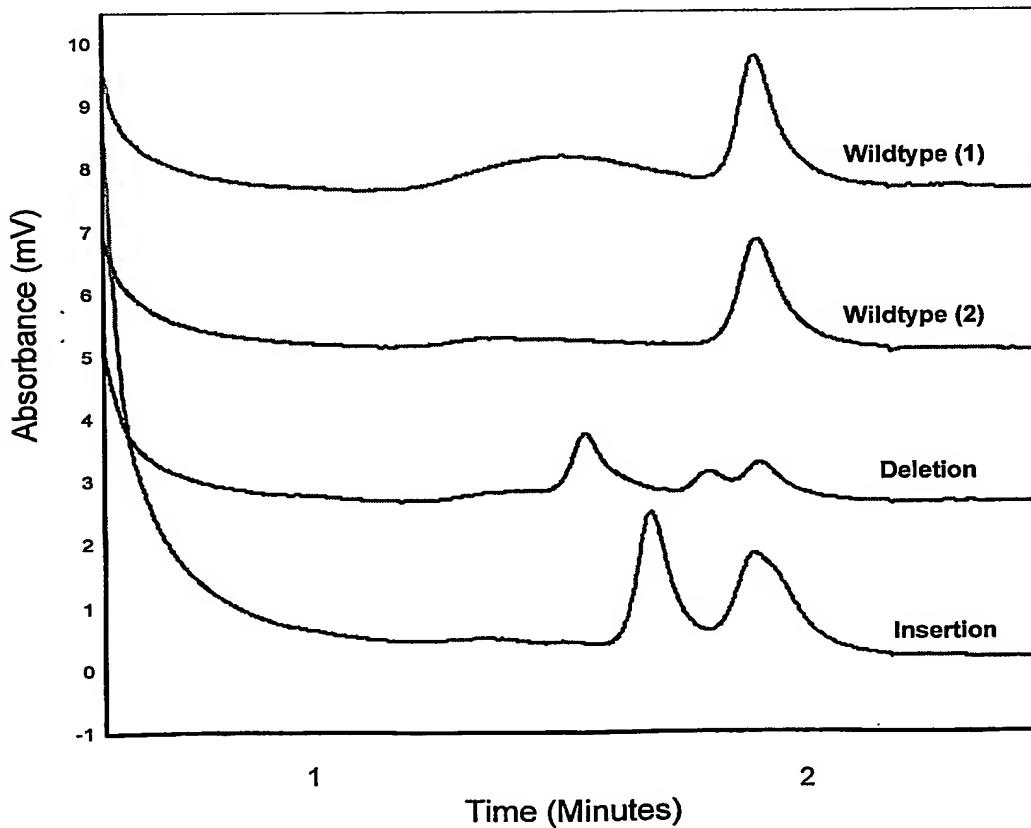
**FIGURE 3**

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**FIGURE 4****BEST AVAILABLE COPY**

**FIGURE 5**

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**FIGURE 6****BEST AVAILABLE COPY**

## FIGURE 7A

181551 GCTTTCTCTC TGTTGGGAGT GGGTGGAGTG AGAACCTGGG AGAAGGCCAG  
CGAAAGAGAG ACAACCCCTCA CCCACCTCAC TCTTGGACCC TCTTCCGGTC  
A F S L L G V G G V R T W E K A S Frame 3

PDGFrA 181534F

181601 CCCTTTATAT CCAGGCAGAC AGCTCCAAGT GCCACCATCG ATCAGCCAGT  
GGAAATATA GGTCCGTCTG TCGAGGTTCA CGGTGGTACC TAGTCGGTCA  
P L Y P G R Q L Q V P P W I S Q S Frame 3

PDGFrA 181640F PDGFrA 181671F

181651 CNTGCAGGGG TGATGCTATT CAGCTACAGA TGGCTTGATC CTGAGTCATT  
GAACGTCCCC ACTACGATAAA GTCGATGTCT ACCGAACTAG GACTCAGTAA  
C R G D A I Q L Q M A \* S \* V I Frame 3

181701 TCTTCCTTTT CCATGCAGTG TGTCCACCGT GATCTGGCTG CTCGCAACGT  
AGAAGGAAAA GGTACGTCAC ACAGGTGGCA CTAGACCGAC GAGCGTTGCA  
S S F S M Q C V H R D L A A R N V Exon 18

Frame 3

PDGFrA 181752F (SNP Exclusion)

181751 CCTCCTGGCA CAAGGAAAAA TTGTGAAGAT CTGTGACTTT GGCCTGGCCA  
GGAGGACCGT GTTCCTTTT AACACTTCTA GACACTGAAA CCGGACCGGT  
L L A Q G K I V K I C D F G L A R Frame 3

181801 GAGACATCAT GCATGATTG AACTATGTGT CGAAAGGCAG TGTACGTCT  
CTCTGTAGTA CGTACTAACG TTGATACACA GCTTCCGTC ACATGCAGGA  
D I M H D S N Y V S K G S V R P Frame 3

PDGFrA 181862R PDGFrA 181874R

181851 CACTCCCTC ACTGGTCAGG CTCATCCTCC TTCACTTAA TCTCTAAAGT  
GTGAAGGGAG TGACCAAGTCC GAGTAGGAGG AAGTGAAATT AGAGATTCA  
H F P H W S G S S S F T L I S K V Frame 3

181901 CAGGTGTTGC TTCTAGAGAT TCGGTGCCCTG TTTTTAAAAA CATCAATAGA  
GTCCACAAACG AAGATCTCTA AGCCACGGAC AAAAAATTTT GTAGTTATCT  
R C C F \* R F G A C F L K H Q \* I Frame 3

**FIGURE 7B**

170551 AAGCATAGCA ACCTAGTTCA GTGCTTGGCA CAGAGAAGGA GCTCAGCAAT  
TTCGTATCGT TGGATCAAGT CACGAACCGT GTCTCTTCCT CGAGTCGTAA  
K H S N L V Q C L A Q R R S S A I Frame 1

PDGFrA 170636F

170601 TACATGTGGA GTGAACGTTG TTGGACTCTA CTGTGTCCAG TCACTGTGCT  
ATGTACACCT CACTGCAAC AACCTGAGAT GACACAGGTC AGTGACACGA  
T C G V N V V G L Y C V Q S L C C Frame 1

PDGFrA 170658F

170651 GCTTCAGTGA AGCTCTGGTG CACTGGACT TTGGTAATTG ACCAGTTACC  
CGAAGTCACT TCGAGACCAAC GTGACCCCTGA AACCATTAAG TGGTCAATGG  
F S E A L V H W D F G N S P V T Frame 1

170701 TGTCCCTGGTC ATTTATAGAA ACCGAGGTAT GAAATTGCTT GGAGGGTCAT  
ACAGGACCAAG TAAATATCTT TGGCTCCATA CTTAAGCGA CCTCCAGTA  
C P G H L \* K P R Y E I R W R V I Exon 12

170751 TGAATCAATC AGCCCAGATG GACATGAATA TATTTATGTT GACCCGATGC  
ACTTAGTTAG TCGGGTCTAC CTGTAATTAT ATAAATACAC CTGGGCTACG  
E S I S P D G H E Y I Y V D P M Q Frame 1

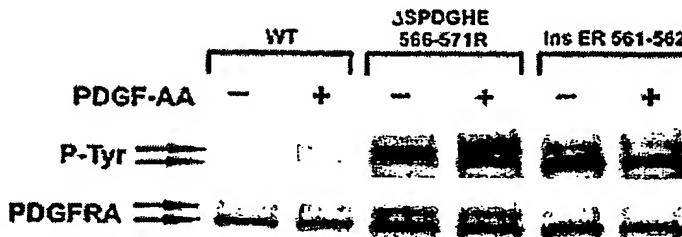
170801 AGCTGCCTTA TGACTCAAGA TGGGAGTTTC CAAGAGATGG ACTAGTGCTT  
TCGACGGAAAT ACTGAGTTCT ACCCTCAAAG GTTCTCTACC TGATCACGAA  
L P Y D S R W E F P R D G L V L Frame 1

PDGFrA 170866R

170851 GGTAAGTTCC ATGGGGTAAC CTCCCAAGAC TCCCTTTTCC CTTGCACACA  
CCATTCAAGG TACCCCATTG GAGGGTTCTG AGGGAAAAGG GAACGTGTGT  
G K F H G V T S Q D S L F P C T Q Frame 1

170901 ACTTTACAAT TTATAGGCCT TGGCAGAATA GAGATCTGAG CTTGTGCTTA  
TGAAATGTAA AATATCCGGA ACCGTCTTAT CTCTAGACTC GAACACGAAT  
L Y N L \* A L A E \* R S E L V L S Frame 1

FIGURE 8

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Exon 12

## Exon 18

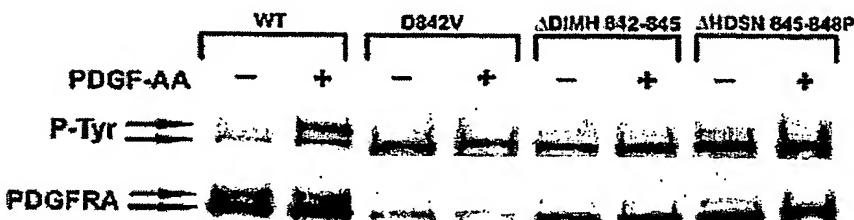
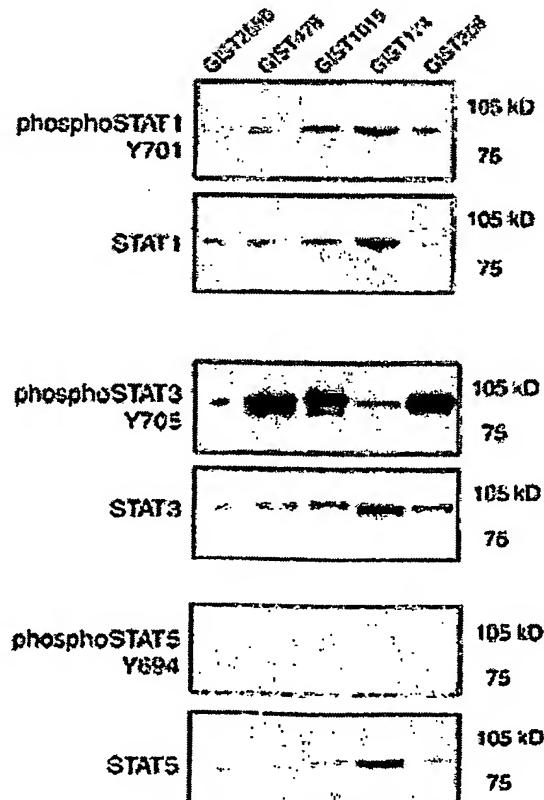
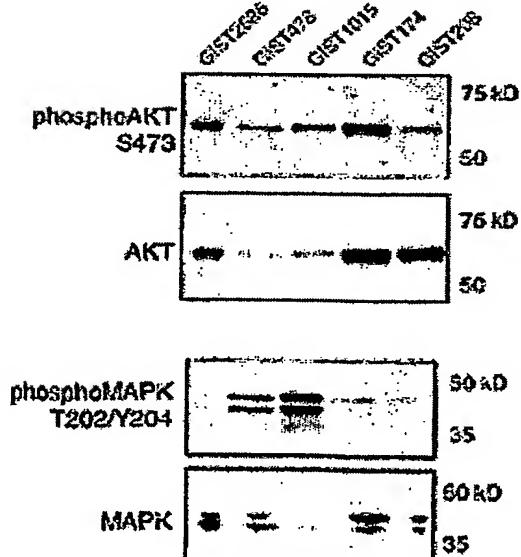


FIGURE 9



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